Access DB# 139 591

# RFE

'TO-1590 (8-01)

#### SEARCH REQUEST FORM

#### Scientific and Technical Information Center

Art Unit: / 635 Phone ?	2 ZARA Number 30 1 - 076 n: 27) 28 Res	Examiner #: 7 + 51.2 Date: // - 30 9  Serial Number: 0 7 / 20 3 / 6 C  Sults Format Preferred (circle): PAPER DISK E-MAIL
$\mathcal{L} (\mathcal{L}, \mathcal{L})$		ize searches in order of need. ***********************************
Please provide a detailed statement of the Include the elected species or structures, l	e search topic, and describe keywords, synonyms, acro s that may have a special n	e as specifically as possible the subject matter to be searched.  onyms, and registry numbers, and combine with the concept or  neaning. Give examples or relevant citations, authors, etc, if
Title of Invention:	utat B)	type,
Inventors (please provide full names):	S v-	les et d.
Earliest Priority Filing Date:	-9-01	
		(parent, child, divisional, or issued patent numbers) along with the
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Online Time:	Other	Other (specify)

Total number of hits satisfying chosen parameters: Scoring table: Sequence: Perfect score: Run on: protein - protein search, using sw model December 1, 2004, 16:20:27; Search time 161 Seconds {without alignments} 1724.574 Million cell updates/sec BLOSUM62 Gapop 10.0 , Gapext 0.5 US-09-803-165-34 4026 2002273 seqs, 358729299 residues MIFDTDYITKDGKPIIRIFK.....KEDLKYQSSKQVGLDAWLKK 774 GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd. 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

geneseqp2002s:\*
geneseqp2003as:\*
geneseqp2003bs:\*
geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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## **ALIGNMENTS**

RESULT 1 AAG78941 ID AAG7 AAG78941; 11-MAR-2000; 2000EP-00105155. 06-MAR-2001; 2001EP-00104583. EP1132474-A1. Thermococcus aggregans Tag polymerase; B-type DNA polymerase. Recombinant Tag DNA polymerase. 13-FBB-2002 (first entry) AAG78941 standard; protein; 774 AA. 12-SEP-2001.

(HOFF ) ROCHE DIAGNOSTICS GMBH.

Sobek H, Frey B, Antranikian G, Boehlke K, Pisani FM, Rossi M;

N-PSDB; AAI70053. WPI; 2001-618367/72.

New thermostable mutant 8-type DNA polymerase with a Y-GG/A amino acid motif between the N-terminal 3'-5' exonuclease domain and the C-terminal polymerase domain in the wild type polymerase, useful for synthesizing nucleic acids.

Disclosure; Fig 9; 40pp; English.

The present invention relates to thermostable mutant B-type DNA polymerases, which have a Y-GG/A amino acid motif between the N-terminal 3'-5' exonuclease domain and the C-terminal polymerase domain, where the tyrosine of this motif is mutated. The mutant B-type DNA polymerase is useful for synthesising nucleic acids and for PCR. The present sequence is the protein sequence for a recombinant Thermococcus aggregans (Tag) DNA polymerase, which was used to illustrate the invention

Sequence 774 AA;

Query Match Best Local Similarity 100.0%; Score 4026; DB 4; Pred. No. 4.2e-305; Length 774;

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                                                                   DSM 10597;
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       MEDLINE=98094267; PubMed=9434178;
Niehaus F., Frey B., Antranikian G.;
Niehaus F., Frey B., Antranikian G.;
"Cloning and characterisation of a thermostable alpha-DNA polymerase from the hyperthermophilic archaeon Thermoccccus sp. TY.";
Gene 204:153-158(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DPOL_THEST STANDARD; PRT; 1829 AA 033845; 15-DEC-1998 (Rel. 37, Created) 15-DEC-1998 (Rel. 37, Last sequence update) 05-JUL-2004 (Rel. 44, Last annotation updat DNA polymerase (EC 2.7.7.7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thermococcus sp. (strain Archaea; Euryarchaeota; Thermococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=110163;
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### ALIGNMENTS

(strain

Thermococci;

Thermococcales; Thermococcaceae;

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EMBL; Y13030; CAA73475.1; -.

REMBL; Y13030; CAA73475.1; -.

InterPro; IPR00612; DNA_pol_B.

InterPro; IPR00613; DNA_pol_B_region.

InterPro; IPR00613; DNA_pol_B_region.

InterPro; IPR006142; INTEIN.

InterPro; IPR006141; Intein_s.

InterPro; IPR006141; Intein_S.

InterPro; IPR006141; Intein_S.

InterPro; IPR006141; Intein_S.

InterPro; IPR0016; DNA_pol_B; 4.

Pfam; PP00116; DNA_pol_B_exo; 1.

PFAM; PF001045; DNA_pol_B_exo; 1.

PRINTS; PR00379; INTEIN_
ITGRPAMG; TIGR01443; Intein_Nterm; 3.

ITGRPAMG; TIGR01445; Intein_Nterm; 3.

ITGRPAMG; TIGR005502; pol_2; 2.

PROSITB; PS00116; DNA_POLYMERASE_B; FALSE_NEG.

PROSITB; PS00116; INTEIN_C_TER; 3.

PROSITB; PS50819; INTEIN_N_TER; 3.

PROSITE; PS50819; INTEIN_N_TER; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as located is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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+ (DNA)(N).

PTM: This protein undergoes a protein self splicing that involves a post-translational excision of the three intervening regions (inteins) followed by peptide ligation.

SIMILARITY: Belongs to the DNA polymerase type-B family.
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STRUCTURES

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Autocatalytic cleavage; DNA replication; DNA-binding;
W DNA-directed DNA polymerase; Endonuclease; Hydrolase;
W Protein splicing; Transferase,
F CHAIN 1 409 DNA polymerase, 1st part (P
F CHAIN 770 855 DNA polymerase, 2nd part (P
F CHAIN 193 1392 Intein II.
F CHAIN 193 1441 DNA polymerase, 3rd part (P
F CHAIN 1142 1598 Intein II.
F CHAIN 1142 1598 Intein III.
F CHAIN 1599 1829 DNA polymerase, 4th part (P
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Best Local Similarity 42.2%;
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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45	44	43	42	41	40	39	38	37	36	ω 5	34	ς, C	32	31	30
500.5	504.5	516	516.5	522.5	527.5	548.5	559.5	570	570.5	578.5	581	583.5	584.5	587	605.5
12.4	12.5	12.8	12.8	13.0	13.1	13.6	13.9	14.2	14.2	14.4	14.4	14.5	14.5	14.6	15.0
913	2154	1405	844	1505	1468	1339	223	1465	959	875	1081	1462	879	1492	1106
N	N	ш	N	2	N	۳	N	ν	N	N	N	щ	N	N	_
T17675	A84669	DJZPA	T31321	S28079	S58250	\$20052	E69125	\$45628	F72763	JC5186	T20698	DJHUAC	A56277	T18560	A39299
	hypothetical prote	DNA	DNA-directed DNA p	-directed DNA	DNA-directed DNA p	DNA-directed DNA p	-dependent			DNA-directed DNA P			DNA-directed DNA P	DNA-directed DNA p	_

## ALIGNMENTS

RESULT 1

A;Cross-references: EMBL:M74198
A;Residues: 181-222;387-425;452-476;483-524;1021-1062;1076-1099;1466-1489;1533-154/ <fe< td=""></fe<>
A; Molecule type: DNA
A; Accession: S42451
A;Reference number: S42450; MJID:92302285; PMID:1608969
A; Title: Intervening sequences in an Archaea DNA polymerase gene.
Proc. Natl. Acad. Sci. U.S.A. 89, 5577-5581, 1992
R;Perler, F.B.; Comb, D.G.; Jack, W.E.; Moran, L.S.; Qiang, B.; Kucera, R.B.; Senner, J
A;Cross-references: UNIPROT:p30317; EMBL:M74198; NID:g154685; PIDN:AAA/Z100.1; P1D:g154
A; Residues: 1-1702 < PER1>
A; Molecule type: DNA
A;Accession: S42459
A;Reference number: S42458
submitted to the EMBL Data Library, September 1992
R;Perler, F.B.; Comb, D.G.; Jack, W.E.; Moran, L.S.; Qiang, B.; Kucera, K.B.; Benner, J
C;Accession: S42459; S42451; S42450; S42458
C;Date: 31-Dec-1993 #sequence_revision 02-Aug-1994 #text_change 09-001-2004
C; Species: Thermococcus litoralis
N; Contains: DNA endonuclease (EC 3.1) PI-I; DNA endonuclease (EC 3.1) PI-II; DNA
DNA-directed DNA polymerase (EC 2.7.7.7) Vent, intein containing precursor - inermotocc
Catalo

R;Hodges, R.A.; Perler, F.B.; Noren, C.J.; Jack, W.E.
Nucleic Acids Res. 20, 6153-6157, 1992
A;Title: Protein splicing removes intervening sequences in an archaea DNA polymerase.
A;Reference number: \$40788; MUID:93117083; PMID:1475179 A; Re A; Mc A; Re A; Ci A; Ti

A;Description: nucleotidyltransferase A;Note: DNA-directed DNA polymerase Vent A; Contents: annotation C; Function: <VENT> ; Punction: <END1>

A,Description: endonuclease; hydrolase A,Note: DNA endonuclease PI-TliI C,Function: <END2>

A;Description: endonuclease; hydrolase
A;Description: endonuclease; hydrolase
A;Note: DNA endonuclease PI-TliII
C;Superfamily: Thermococcus litoralis DNA-directed DNA polymerase Vent
C;Keywords: DNA binding; endonuclease; hydrolase; nucleotidyltransferase; protein splic
F;1-494,1033-1081,1472-1702/product: DNA-directed DNA polymerase Vent #status predicted
F;1-494/Domain: DNA-directed DNA polymerase Vent extein 1 #status predicted <ATI>
F;495-1032/product: DNA endonuclease PI-II (pol Vent intein 2 #status predicted <ATI>
F;1033-1081/Domain: DNA-directed DNA polymerase Vent extein 2 #status predicted <ATI>
F;1082-1471/Product: DNA endonuclease PI-I (pol Vent intein 2) #status predicted <ATI>
F;1081-1472/TO2/Domain: DNA-directed DNA polymerase Vent extein 3 #status predicted <ATI>
F;40470-1702/Domain: DNA-directed DNA polymerase Vent extein 3 #status predicted <ATI>
F;4041-1033/Cross-link: peptide (Asn-Ser) #status predicted
F;1081-1472/Cross-link: peptide (Asn-Ser) #status predicted

Matches Local 726; Similarity Conservative 83.4%; 42.7%; Score 3356; DB 2; Pred. No. 3.8e-166; 3; Mismatches 15; Length 1702; Indels 928; Gaps 2

901 VFILNSLGISSVKIGFDSGVYRVYINEDLQFPQTSREKNTYYSNLIPKBILRDVFGKEFQ 960 494	494	
Ouery Match  79.6%; Score 3204.5; DB 2; Length 775;  Best Local Similarity 76.6%; Pred. No. 9.4e-159;  Matches 592; Conservative 89; Mismatches 89; Indels 3; Gaps 2;  Matches 592; Conservative 89; Mismatches 89; Indels 3; Gaps 2;  Matches 592; Conservative 89; Mismatches 89; Indels 3; Gaps 2;  Matches 592; Conservative 89; Mismatches 3; Gaps 2;  Matches 592; Mismatches 89; Mismatches 89; Indels 3; Gaps 2;  Matches 592; Mismatches 89; Mismatches 89; Indels 3; Gaps 2;  Matches 592; Mismatches 89; Mismatches 89; Indels 3; Gaps 2;  Matches 592; Mismatches 89; Mismatches 89; Indels 3; Gaps 2;  Matches 592; Mismatches 89; Mismatches 89; Indels 3; Gaps 2;  Matches 592; Mismatches 89; Mismatches 89; Indels 3; Gaps 2;  Matches 592; Mismatches 89; Mismatches 89; Indels 3; Gaps 2;  Matches 592; Mismatches 89; Mismatches 89; Indels 3; Gaps 2;  Matches 592; Mismatches 89; Mismatches 89; Indels 3; Gaps 2;  Matches 592; Mismatches 89; Mismatches 89; Indels 3; Gaps 2;  Matches 592; Mismatches 89; Mismatches 89; Indels 89; In	RESULT 2 S67920 DNA-directed DNA polymerase (EC 2.7.7.7) - Thermococcus sp. C;Species: Thermococcus sp. C;Species: Thermococcus sp. C;Date: 17-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 09-Jul-2004 C;Accession: S67920 C;Accession: S67920 R;Southworth, M.S.; Kong, H.; Kucera, R.B.; Ware, J.; Jannasch, H.W.; Perler, F.B. submitted to the EMBL Data Library, January 1996 A;Description: Cloning, expression and modulation of the 3'-5' exonuclease activity of A;Reference number: S67920 A;Accession: S67920 A;Accession: S67920 A;Molecule type: DNA A;Residues: 1-775 <80U> A;Cross-references: UNIPROT:Q56366; GB:U47108; NID:g1197451; PIDN:AAA888769.1; PID:g1197 A;Experimental source: strain 90N-7 C;Superfamily: DNA polymerase C;Keywords: DNA binding; nucleotidyltransferase	

B ð